

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/594,118
Source: FWP
Date Processed by STIC: 10/11/06

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/594,118

CRF Edit Date: 10/11/06
Edited by: KZ

___ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

___ Corrected the SEQ ID NO. Sequence numbers edited were:

___ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

✓ Deleted: ✓ invalid beginning/end-of-file text ; ___ page numbers

___ Inserted mandatory headings/numeric identifiers, specifically:

___ Moved responses to same line as heading/numeric identifier, specifically:

___ Other:



IFWP

RAW SEQUENCE LISTING

DATE: 10/11/2006

PATENT APPLICATION: US/10/594,118

TIME: 15:22:10

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\10112006\J594118.raw

```

2 <110> APPLICANT: Golz, Stefan
3      Bruggemeier, Ulf
4      Geerts, Andrease
6 <120> TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
7      Peroxisome Proliferator Activated Receptor Delta (PPARD)
W--> 8 <130> FILE REFERENCE: 004974.01218
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/594,118
C--> 10 <141> CURRENT FILING DATE: 2006-09-25
10 <150> PRIOR APPLICATION NUMBER: PCT/EP2005/002529
11 <151> PRIOR FILING DATE: 2005-03-10
13 <150> PRIOR APPLICATION NUMBER: EP 04007020.3
14 <151> PRIOR FILING DATE: 2004-03-24
16 <160> NUMBER OF SEQ ID NOS: 5
17 <170> SOFTWARE: PatentIn version 3.2
W--> 18 <210> SEQ ID NO: 1
19 <211> LENGTH: 3301
20 <212> TYPE: DNA
21 <213> ORGANISM: Homo sapiens
W--> 22 <220> FEATURE:
23 <221> NAME/KEY: misc_feature
24 <222> LOCATION: (2966)..(2972)
25 <223> OTHER INFORMATION: n is a, c, g, or t
W--> 26 <400> SEQUENCE: 1
27 gaattctgcg gagcctgcgg gacggcgcg ggttgggccg taggcagccg ggacagtgtt      60
28 gtacagtgtt ttgggcatgc acgtgatact cacacagtgg cttctgctca ccaacagatg      120
29 aagacagatg caccaacgag ggtctggaat ggtctggagt ggtctggaaa gcagggtcag      180
30 atacccttgg aaaactgaag cccgtggagc aatgatctct acaggactgc ttcaaggctg      240
31 atgggaacca cctgttagag gtccatctgc gttcagaccc agacgatgcc agagctatga      300
32 ctgggcctgc aggtgtggcg ccgaggggag atcagccatg gagcagccac aggaggaagc      360
33 ccctgaggtc cggaagagg aggagaaaga ggaagtggca gaggcagaag gagccccaga      420
34 gtcfaatggg ggaccacagc atgcacttcc ttccagcagc tacacagacc tctcccggag      480
35 ctccctgcca cctcactgct tggaccaact gcagatgggc tgtgacgggg cctcatgctg      540
36 cagcctcaac atggagtgcc ggggtgtgctg ggacaaggca tcgggcttcc actacggtgt      600
37 tcatgcatgt gaggggtgca agggcttctt ccgtcgtacg atccgcatga agctggagta      660
38 cgagaagtgt gagcgagct gcaagattca gaagaagaac cgcaacaagt gccagtactg      720
39 ccgcttccag aagtgcctgg cactgggcat gtcacacaac gctatccgtt ttggtcggat      780
40 gccggaggct gagaagagga agctggtggc agggctgact gcaaacgagg ggagccagta      840
41 caacccacag gtggccgacc tgaaggcctt ctccaagcac atctacaatg cctacctgaa      900
42 aaacttcaac atgacaaaaa agaaggcccg cagcatcctc accggcaaaag ccagccacac      960
43 ggcgcccttt gtgatccacg acatcgagac attgtggcag gcagagaagg ggctggtgtg      1020
44 gaagcagttg gtgaatggcc tgccctcccta caaggagatc agcgtgcacg tcttctaccg      1080
45 ctgccagtgc accacagtgg agaccgtgct ggagctcaat gagttcgcca agagcatccc      1140
46 cagcttcagc agcctcttcc tcaacgacca ggttaccctt ctcaagtatg gcgtgcacga      1200

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```

47 ggccatcttc gccatgctgg cctctatcgt caacaaggac gggctgctgg tagccaacgg 1260
48 cagtggcttt gtcacccgtg agttcctgcg cagcctccgc aaacccttca gtgatatcat 1320
49 tgagcctaag tttgaatttg ctgtcaagtt caacgccctg gaacttgatg acagtgcact 1380
50 ggccctattc attgcgcca tcattctgtg tggagaccgg ccaggcctca tgaacgttcc 1440
51 acgggtggag gctatccagg acaccatcct gcgtgccctc gaattccacc tgcaggccaa 1500
52 ccaccctgat gcccagtagc tcttccccaa gctgctgcag aagatggctg acctgcgga 1560
53 actggtcacc gagcacgccc agatgatgca gcggatcaag aagaccgaaa ccgagacctc 1620
54 gctgcaccct ctgctccagg agatctacaa ggacatgtac taacggcggc acccaggcct 1680
55 ccctgcagac tccaatgggg ccagcactgg aggggcccac ccacatgact tttccattga 1740
56 ccagctctct tccctgtctt gttgtctccc tctttctcag ttcctctttc ttttctaatt 1800
57 cctgttgctc tgtttcttcc tttctgtagg tttctctctt cccttctccc ttctcccttg 1860
58 ccctcccttt ctctctccta tccccacgtc tgctctcctt tcttattctg tgagatgttt 1920
59 tgtattattt caccagcagc atagaacagg acctctgctt ttgcacacct tttccccagg 1980
60 agcagaagag agtgggcttg ccctctgccc catcattgca cctgcaggct taggtcctca 2040
61 cttctgtctc ctgtcttcag agcaaaagac ttgagccatc caaagaaaca ctaagctctc 2100
62 tgggcctggg ttcaggga ggctaagcat ggctggact gactgcagcc ccctatagtc 2160
63 atggggtccc tgctgcaaag gacagtggca gaccccgga gtagagccga gatgcctccc 2220
64 caagactgtc attgcccctc cgatcgtgag gccaccact gacccaatga tctctccag 2280
65 cagcacacct cagccccact gacaccagc gtccttccat cttcacactg gtttgccagg 2340
66 ccaatgttgc tgatggcccc tccagcacac acacataagc actgaaatca ctttacctgc 2400
67 aggaccatg cacctccctt ccctccctga ggcaggtag aaccagaga gaggggctg 2460
68 caggtgagca ggcagggtg ggcagggtc cggggaggc aggggtctg caggctctg 2520
69 tgggtcagcc cagcacctg ccagtgga gcttcccg ataaactgag cctgttcatt 2580
70 ctgatgtcca tttgtcccaa tagctctact gccctccct tcccccttac tcagcccagc 2640
71 tggccacctc gaagtctccc tgcacagcct ctagtgtccg gggacctgtg gggaccagtc 2700
72 ccacaccgct ggtccctgcc ctcccctgct ccaggttga ggtgcgctca cctcagagca 2760
73 gggccaaagc acagctgggc atgccatgtc tgagcgggc agagccctcc aggcctgcag 2820
74 gggcaagggg ctggtggag tctcagagca cagaggtagg agaactgggg ttcaagccca 2880
75 ggcttctctg gtcctgctg gtcctccctc ccaaggagcc attctatgtg actctgggtg 2940
W--> 76 gaagtgccea gcccctgct gacggnnnnn nngatcactc tctgctggca ggattcttcc 3000
77 cgtcccccac ctaccagct gatgggggtt ggggtgcttc tttcagccaa ggctatgaag 3060
78 ggacagctgc tgggaccac ctccccctt ccccgccac atgccgcgtc cctgccccca 3120
79 cccgggtctg gtgctgagga tacagctctt ctcagtgtct gaacaatctc caaaattgaa 3180
80 atgtatattt ttgctaggag cccagcttc ctgtgtttt aatataaata gtgtacacag 3240
81 actgacgaaa ctttaaataa atgggaatta aatatttaaa aaaaaagcg gccgcgaatt 3300
82 c 3301
83 <210> SEQ ID NO: 2
84 <211> LENGTH: 441
85 <212> TYPE: PRT
86 <213> ORGANISM: Homo sapiens
W--> 87 <400> SEQUENCE: 2
88 Met Glu Gln Pro Gln Glu Glu Ala Pro Glu Val Arg Glu Glu Glu Glu
89 1 5 10 15
90 Lys Glu Glu Val Ala Glu Ala Glu Gly Ala Pro Glu Leu Asn Gly Gly
91 20 25 30
92 Pro Gln His Ala Leu Pro Ser Ser Ser Tyr Thr Asp Leu Ser Arg Ser
93 35 40 45
94 Ser Ser Pro Pro Ser Leu Leu Asp Gln Leu Gln Met Gly Cys Asp Gly
95 50 55 60

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```

96 Ala Ser Cys Gly Ser Leu Asn Met Glu Cys Arg Val Cys Gly Asp Lys
97 65                      70                      75                      80
98 Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly
99                      85                      90                      95
100 Phe Phe Arg Arg Thr Ile Arg Met Lys Leu Glu Tyr Glu Lys Cys Glu
101                      100                      105                      110
102 Arg Ser Cys Lys Ile Gln Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys
103                      115                      120                      125
104 Arg Phe Gln Lys Cys Leu Ala Leu Gly Met Ser His Asn Ala Ile Arg
105                      130                      135                      140
106 Phe Gly Arg Met Pro Glu Ala Glu Lys Arg Lys Leu Val Ala Gly Leu
107 145                      150                      155                      160
108 Thr Ala Asn Glu Gly Ser Gln Tyr Asn Pro Gln Val Ala Asp Leu Lys
109                      165                      170                      175
110 Ala Phe Ser Lys His Ile Tyr Asn Ala Tyr Leu Lys Asn Phe Asn Met
111                      180                      185                      190
112 Thr Lys Lys Lys Ala Arg Ser Ile Leu Thr Gly Lys Ala Ser His Thr
113                      195                      200                      205
114 Ala Pro Phe Val Ile His Asp Ile Glu Thr Leu Trp Gln Ala Glu Lys
115                      210                      215                      220
116 Gly Leu Val Trp Lys Gln Leu Val Asn Gly Leu Pro Pro Tyr Lys Glu
117 225                      230                      235                      240
118 Ile Ser Val His Val Phe Tyr Arg Cys Gln Cys Thr Thr Val Glu Thr
119                      245                      250                      255
120 Val Arg Glu Leu Thr Glu Phe Ala Lys Ser Ile Pro Ser Phe Ser Ser
121                      260                      265                      270
122 Leu Phe Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu
123                      275                      280                      285
124 Ala Ile Phe Ala Met Leu Ala Ser Ile Val Asn Lys Asp Gly Leu Leu
125                      290                      295                      300
126 Val Ala Asn Gly Ser Gly Phe Val Thr Arg Glu Phe Leu Arg Ser Leu
127 305                      310                      315                      320
128 Arg Lys Pro Phe Ser Asp Ile Ile Glu Pro Lys Phe Glu Phe Ala Val
129                      325                      330                      335
130 Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Leu Phe Ile
131                      340                      345                      350
132 Ala Ala Ile Ile Leu Cys Gly Asp Arg Pro Gly Leu Met Asn Val Pro
133                      355                      360                      365
134 Arg Val Glu Ala Ile Gln Asp Thr Ile Leu Arg Ala Leu Glu Phe His
135                      370                      375                      380
136 Leu Gln Ala Asn His Pro Asp Ala Gln Tyr Leu Phe Pro Lys Leu Leu
137 385                      390                      395                      400
138 Gln Lys Met Ala Asp Leu Arg Gln Leu Val Thr Glu His Ala Gln Met
139                      405                      410                      415
140 Met Gln Arg Ile Lys Lys Thr Glu Thr Glu Thr Ser Leu His Pro Leu
141                      420                      425                      430
142 Leu Gln Glu Ile Tyr Lys Asp Met Tyr
143                      435                      440
144 <210> SEQ ID NO: 3

```

RAW SEQUENCE LISTING

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Input Set : A:\PTO.AMC.txt

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```
145 <211> LENGTH: 19
146 <212> TYPE: DNA
147 <213> ORGANISM: artificial sequence
W--> 148 <220> FEATURE:
149 <223> OTHER INFORMATION: forward primer
W--> 150 <400> SEQUENCE: 3
151 cagtactgcc gcttcaga 19
152 <210> SEQ ID NO: 4
153 <211> LENGTH: 20
154 <212> TYPE: DNA
155 <213> ORGANISM: artificial sequence
W--> 156 <220> FEATURE:
157 <223> OTHER INFORMATION: reverse primer
W--> 158 <400> SEQUENCE: 4
159 catccgacca aaacggatag 20
160 <210> SEQ ID NO: 5
161 <211> LENGTH: 24
162 <212> TYPE: DNA
163 <213> ORGANISM: artificial sequence
W--> 164 <220> FEATURE:
165 <223> OTHER INFORMATION: probe
W--> 166 <400> SEQUENCE: 5
167 ctggcactgg gcatgtcaca caac 24
```

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/594,118

DATE: 10/11/2006
TIME: 15:22:11

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\10112006\J594118.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 2966,2967,2968,2969,2970,2971,2972

VERIFICATION SUMMARY

DATE: 10/11/2006

PATENT APPLICATION: US/10/594,118

TIME: 15:22:11

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\10112006\J594118.raw

L:8 M:283 W: Missing Blank Line separator, <130> field identifier
L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:18 M:283 W: Missing Blank Line separator, <210> field identifier
L:22 M:283 W: Missing Blank Line separator, <220> field identifier
L:26 M:283 W: Missing Blank Line separator, <400> field identifier
L:76 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:2940
L:87 M:283 W: Missing Blank Line separator, <400> field identifier
L:148 M:283 W: Missing Blank Line separator, <220> field identifier
L:150 M:283 W: Missing Blank Line separator, <400> field identifier
L:156 M:283 W: Missing Blank Line separator, <220> field identifier
L:158 M:283 W: Missing Blank Line separator, <400> field identifier
L:164 M:283 W: Missing Blank Line separator, <220> field identifier
L:166 M:283 W: Missing Blank Line separator, <400> field identifier